



SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Therapeutic agent for diseases caused by PTH or PTHrP

<130> 04853.0086

<140> US 10/019,571

<141> 2001-12-31

<150> PCT/JP00/04414

<151> 2000-07-03

<150> JP 11-189793

<151> 1999-07-02

<160> 76

<170> PatentIn version 3.1

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35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Ser Ile Ser
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Asn Ile Gln Pro Glu Asp Glu Ala Met Tyr Ile Cys Gly Val Gly Asp
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Thr Val Leu Gly Gln Pro
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<213> Mus musculus

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35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
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Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys
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20 25 30

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35 40 45

Lys Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp
85 90 95

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu Gly
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20 25 30

Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys Tyr Leu Met
35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser

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Thr Val Leu Gly Gln Pro			
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Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys Tyr Val Met			
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Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser			
65	70	75	80
Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp			
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Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu			
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Thr Val Leu Gly Gln Pro			
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35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp
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Thr Val Leu Gly Gln Pro
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35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp
85 90 95

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100 105 110

Thr Val Leu Gly Gln Pro
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20 25 30

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35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser

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Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp			
85	90	95	
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu			
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Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp			
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Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser			
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Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp			
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35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
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Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp
85 90 95

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu Gly Gln Pro
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20 25 30

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35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp
85 90 95

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100 105 110

Thr Val Leu Gly Gln Pro
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35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65	70	75	80
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Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly Gln Gly Thr			
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Leu Val Thr Val Ser Ser			
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cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc		144	
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe			
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Ser Ser Tyr Gly Met Ser Trp Ile Arg Gln Thr Pro Asp Lys Arg Leu			
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Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro			
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gac agt gtg aag ggg cga ttc acc atc tcc aga gac aat gcc aag aac		288	

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn			
65	70	75	
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Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met			
80	85	90	
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Phe Tyr Cys Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly			
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Gln Gly Thr Leu Val Thr Val Ser Ala			
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Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro			
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Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
80	85
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Tyr Tyr Cys Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly	
95	100
	105
cag gga acc ctg gtc acc gtc tcc tca	411
Gln Gly Thr Leu Val Thr Val Ser Ser	
110	115
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Lys Ala Ser Gln Asp Val Asn Thr Ala Val Ala	
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Ser Ala Ser Asn Arg Tyr Thr	
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Gln Gln His Tyr Ser Thr Pro Phe Thr	
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<212> PRT
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<400> 62

Pro Tyr Trp Met Gln
1 5

<210> 63
<211> 16
<212> PRT
<213> Homo sapiens

<400> 63

Ser Ile Phe Gly Asp Gly Asp Thr Arg Tyr Ser Gln Lys Phe Lys Gly
1 5 10 15

<210> 64
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<400> 64

Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 65
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Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly
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tct ttc tcc caa ctt gtg ctc act cag tca tct tca gcc tct ttc tcc 96

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc	96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser	
-1 1 5 10	
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt	144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser	
15 20 25	
acg tac acc att gaa tgg cat cag cag cca gag aag ggc cct cg	192
Thr Tyr Thr Ile Glu Trp His Gln Gln Pro Glu Lys Gly Pro Arg	
30 35 40 45	
tac ttg atg aaa ctt aag caa gat gga agc cac agc aca ggt gat ggg	240
Tyr Leu Met Lys Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly	
50 55 60	
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc	288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu	
65 70 75	
acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt	336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly	
80 85 90	
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg	384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly	
95 100 105	
acc aaa ctg acc gtc cta ggt cag ccc	411
Thr Lys Leu Thr Val Leu Gly Gln Pro	
110 115	
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atg gcc tgg act cct ctc ttc ttc ttc gtt ctt cat tgc tca ggt	48
Met Ala Trp Thr Pro Leu Phe Phe Phe Phe Val Leu His Cys Ser Gly	
-15 -10 -5	

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc	96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser	
-1 1 5 10	
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt	144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser	
15 20 25	
acg tac acc att gaa tgg tat cag cag cca gag aag ggc cct aag	192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys	
30 35 40 45	
tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg	240
Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly	
50 55 60	
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc	288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu	
65 70 75	
acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt	336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly	
80 85 90	
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg	384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly	
95 100 105	
acc aaa ctg acc gtc cta ggc cag ccc	411
Thr Lys Leu Thr Val Leu Gly Gln Pro	
110 115	
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atg gcc tgg act cct ctc ttc ttc ttc ttt gtt ctt cat tgc tca ggt	48
Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly	

Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly			
	-15	-10	-5
tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc			96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser			
-1 1 5 10			
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt			144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser			
15 20 25			
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct agg			192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg			
30 35 40 45			
tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg			240
Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly			
50 55 60			
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc			288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu			
65 70 75			
acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt			336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly			
80 85 90			
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg			384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly			
95 100 105			
acc aaa ctg acc gtc cta ggc cag ccc			411
Thr Lys Leu Thr Val Leu Gly Gln Pro			
110 115			

<210> 70
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tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc	96		
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser			
-1	1	5	
.	10	
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt	144		
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser			
15	20	25	
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct agg	192		
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg			
30	35	40	45
tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg	240		
Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly			
50	55	60	
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc	288		
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu			
65	70	75	
acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt	336		
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly			
80	85	90	
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg	384		
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly			
95	100	105	
acc aaa ctg acc gtc cta ggc cag ccc	411		
Thr Lys Leu Thr Val Leu Gly Gln Pro			
110	115		

<210> 71
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<212> DNA
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Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly			
-15	-10	-5	
tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc			96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser			
-1	1	5	10
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt			144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser			
15	20	25	
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag			192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Lys			
30	35	40	45
tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg			240
Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly			
50	55	60	
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc			288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu			
65	70	75	
acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt			336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly			
80	85	90	
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg			384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly			
95	100	105	
acc aaa ctg acc gtc cta ggc cag ccc			411
Thr Lys Leu Thr Val Leu Gly Gln Pro			
110	115		

<210> 72
<211> 411
<212> DNA
<213> Homo sapiens

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<400>	72		
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Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly			
-15	-10	-5	
tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc			96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser			
-1 1 5 10			
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt			144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser			
15 20 25			
acg tac acc att gaa tgg tat cag cag cca gag aag ggc cct agg			192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg			
30 35 40 45			
tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg			240
Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly			
50 55 60			
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc			288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu			
65 70 75			
acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt			336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly			
80 85 90			
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg			384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly			
95 100 105			
acc aaa ctg acc gtc cta ggc cag ccc			411
Thr Lys Leu Thr Val Leu Gly Gln Pro			
110 115			

<210> 73
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 <212> DNA
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<220>
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<400> 73
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-15 -10 -5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser
-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser
15 20 25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag 192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys
30 35 40 45

tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240
Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly
50 55 60

att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu
65 70 75

acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt 336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly
80 85 90

gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly
95 100 105

acc aaa ctg acc gtc cta ggc cag ccc 411
Thr Lys Leu Thr Val Leu Gly Gln Pro
110 115

<210> 74
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tct ttc tcc cag ctt gtg ctg actcaa tcg ccc tct gcc tct gcc tcc				96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser				
-1 1 5		10		
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt				144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser				
15 20 25				
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct agg				192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg				
30 35 40 45				
tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg				240
Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly				
50 55 60				
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc				288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu				
65 70 75				
acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt				336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly				
80 85 90				
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg				384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly				
95 100 105				
acc aaa ctg acc gtc cta ggc cag ccc				411
Thr Lys Leu Thr Val Leu Gly Gln Pro				
110 115				

<210> 75

<211> 34

<212> PRT

<213> Homo sapiens

<400> 75

Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln				
1 5 10 15				

Asp	Leu	Arg	Arg	Arg	Phe	Phe	Leu	His	His	Leu	Ile	Ala	Glu	Ile	His
		20					25					30			

Thr Ala

<210>	76
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<212>	DNA
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<220>	
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<223>	

<400>	76																	
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											Met	Gly	Thr	Ala	Arg	Ile	Ala	Pro
											1						5	
ggc	ctg	gcg	ctc	ctg	ctc	tgc	tgc	ccc	gtg	ctc	agc	tcc	g	cg	tac	gc	g	100
Gly	Leu	Ala	Leu	Leu	Leu	Cys	Cys	Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala			
10						15				20								
ctg	gtg	gat	gca	gat	gac	gtc	atg	act	aaa	gag	gaa	cag	atc	ttc	ctg		148	
Leu	Val	Asp	Ala	Asp	Asp	Val	Met	Thr	Lys	Glu	Glu	Gln	Ile	Phe	Leu			
25						30				35							40	
ctg	cac	cgt	gct	cag	gcc	cag	tgc	gaa	aaa	cgg	ctc	aag	gag	gtc	ctg		196	
Leu	His	Arg	Ala	Gln	Ala	Gln	Cys	Glu	Lys	Arg	Leu	Lys	Glu	Val	Leu			
										45		50					55	
cag	agg	cca	gcc	agc	ata	atg	gaa	tca	gac	aag	gga	tgg	aca	tct	gc		244	
Gln	Arg	Pro	Ala	Ser	Ile	Met	Glu	Ser	Asp	Lys	Gly	Trp	Thr	Ser	Ala			
						60				65							70	
tcc	aca	tca	ggg	aag	ccc	agg	aaa	gat	aag	gca	tct	ggg	aag	ctc	ta		292	
Ser	Thr	Ser	Gly	Lys	Pro	Arg	Lys	Asp	Lys	Ala	Ser	Gly	Lys	Leu	Tyr			
						75				80							85	
cct	gag	tct	gag	gag	gac	aag	gag	gca	ccc	act	ggc	agc	agg	ta	cg		340	
Pro	Glu	Ser	Glu	Asp	Lys	Glu	Ala	Pro	Thr	Gly	Ser	Arg	Tyr	Arg				
						90				95							100	
ggg	cgc	ccc	tgt	ctg	ccg	gaa	tgg	gac	cac	atc	ctg	tgc	tgg	ccg	ctg		388	
Gly	Arg	Pro	Cys	Leu	Pro	Glu	Trp	Asp	His	Ile	Leu	Cys	Trp	Pro	Leu			
105						110				115							120	
ggg	gca	cca	ggt	gag	gtg	gtg	gct	gtg	ccc	tgt	ccg	gac	ta	tt	at		436	

Gly Ala Pro Gly Glu Val Val Ala Val Pro Cys Pro Asp Tyr Ile Tyr			
125	130	135	
gac ttc aat cac aaa ggc cat gcc tac cga cgc tgt gac cgc aat ggc			484
Asp Phe Asn His Lys Gly His Ala Tyr Arg Arg Cys Asp Arg Asn Gly			
140	145	150	
agc tgg gag ctg gtg cct ggg cac aac agg acg tgg gcc aac tac agc			532
Ser Trp Glu Leu Val Pro Gly His Asn Arg Thr Trp Ala Asn Tyr Ser			
155	160	165	
gag tgt gtc aaa ttt ctc acc aat gag act cgt gaa cg ^g gag gtg ttt			580
Glu Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe			
170	175	180	
gac cgc ctg ggc atg att tac acc gtg ggc tac tcc gtg tcc ctg gcg			628
Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala			
185	190	195	200
tcc ctc acc gta gct gtg ctc atc ctg gcc tac ttt agg cg ^g ctg cac			676
Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His			
205	210	215	
tgc acg cgc aac tac atc cac atg cac ctg ttc ctg tcc ttc atg ctg			724
Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met Leu			
220	225	230	
cgc gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc gcc			772
Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala			
235	240	245	
acg ctt gat gag gct gag cg ^c ctc acc gag gag ctg cg ^c gcc atc			820
Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Leu Arg Ala Ile			
250	255	260	
gcc cag gcg ccc ccg ccg cct gcc acc gcc gct gcc ggc tac gcg ggc			868
Ala Gln Ala Pro Pro Pro Ala Thr Ala Ala Gly Tyr Ala Gly			
265	270	275	280
tgc agg gtg gct gtg acc ttc ttc ctt tac ttc ctg gcc acc aac tac			916
Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr			
285	290	295	
tac tgg att ctg gtg gag ggg ctg tac ctg cac agc ctc atc ttc atg			964
Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met			
300	305	310	
gcc ttc ttc tca gag aag aag tac ctg tgg ggc ttc aca gtc ttc ggc			1012
Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly			
315	320	325	
tgg ggt ctg ccc gct gtc ttc gtg gct gtg tgg gtc agt gtc aga gct			1060

Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg Ala			
330	335	340	
acc ctg gcc aac acc ggg tgc tgg gac ttg agc tcc ggg aac aaa aag			1108
Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys			
345	350	355	360
tgg atc atc cag gtg ccc atc ctg gcc tcc att gtg ctc aac ttc atc			1156
Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe Ile			
365	370	375	
ctc ttc atc aat atc gtc cggtg ctc gcc acc aag cag cggtg gag acc			1204
Leu Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Gln Arg Glu Thr			
380	385	390	
aac gcc ggc cggtgt gac aca cggtg cag tac cggtg aag ctg ctc aaa			1252
Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys			
395	400	405	
tcc acg ctg gtg ctc atg ccc ctc ttt ggc gtc cac tac att gtc ttc			1300
Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe			
410	415	420	
atg gcc aca cca tac acc gag gtc tca ggg acg ctc tgg caa gtc cag			1348
Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val Gln			
425	430	435	440
atg cac tat gag atg ctc ttc aac tcc ttc cag gga ttt ttt gtc gca			1396
Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala			
445	450	455	
atc ata tac tgt ttc tgc aat ggc gag gta caa gct gag atc aag aaa			1444
Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys			
460	465	470	
tct tgg agc cgc tgg aca ctg gca ctg gac ttc aag cga aag gca cgc			1492
Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg			
475	480	485	
agc ggg agc agc agc tat agc tac ggc ccc atg gtg tcc cac aca agt			1540
Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser			
490	495	500	
gtg acc aat gtc ggc ccc cgt gtg gga ctc ggc ctg ccc ctc agc ccc			1588
Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro			
505	510	515	520
cgc cta ctg ccc act gcc acc acc aac ggc cac cct cag ctg cct ggc			1636
Arg Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro Gly			
525	530	535	
cat gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca cca			1684

His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro			
540	545	550	
cct gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc tgc			1732
Pro Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys			
555	560	565	
tca ggc ctg gac gag gag gcc tct ggg cct gag cg ^g cca cct gcc ctg			1780
Ser Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu			
570	575	580	
cta cag gaa gag tgg gag aca gtc atg tga			1810
Leu Gln Glu Glu Trp Glu Thr Val Met			
585	590		